

D. Krose

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[Handwritten signature]



1638

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/697,719

DATE: 05/21/2002

TIME: 13:32:37

Input Set : A:\0020-4764P.st25A.txt

Output Set: N:\CRF3\05212002\I697719.raw

P.6

3 <110> APPLICANT: NAKAJIMA, Hiroki
4 NAGASAWA, Akitsu
6 <120> TITLE OF INVENTION: Method for giving resistance to weed control compounds to plants

ENTERED

8 <130> FILE REFERENCE: 0020-4764P
10 <140> CURRENT APPLICATION NUMBER: 09/697,719
11 <141> CURRENT FILING DATE: 2000-10-27
13 <150> PRIOR APPLICATION NUMBER: JP 10/120553
14 <151> PRIOR FILING DATE: 1998-04-30
16 <150> PRIOR APPLICATION NUMBER: JP 10/281127
17 <151> PRIOR FILING DATE: 1998-10-02
19 <150> PRIOR APPLICATION NUMBER: JP 10/330981
20 <151> PRIOR FILING DATE: 1998-11-20
22 <150> PRIOR APPLICATION NUMBER: JP 11/054730
23 <151> PRIOR FILING DATE: 1999-03-02
25 <160> NUMBER OF SEQ ID NOS: 78
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 39
29 <212> TYPE: DNA
30 <213> ORGANISM: Artificial Sequence
32 <220> FEATURE:
33 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify bchH gene
35 <400> SEQUENCE: 1
36 gacatctaga ggagacgacc atatgcacgg tgaagtctc 39
38 <210> SEQ ID NO: 2
39 <211> LENGTH: 31
40 <212> TYPE: DNA
41 <213> ORGANISM: Artificial Sequence
43 <220> FEATURE:
44 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify bchH gene
46 <400> SEQUENCE: 2
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49 <210> SEQ ID NO: 3
50 <211> LENGTH: 39
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify soybean PPO gene
57 <400> SEQUENCE: 3
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60 <210> SEQ ID NO: 4
61 <211> LENGTH: 36
62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial Sequence

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65 <220> FEATURE:
66 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify soybean PPO gene
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72 <211> LENGTH: 1632
73 <212> TYPE: DNA
74 <213> ORGANISM: Glycine max var. Williams82
76 <220> FEATURE:
77 <221> NAME/KEY: CDS
78 <222> LOCATION: (1)...(1632)
80 <400> SEQUENCE: 5
81 atg gtt tcc gtc ttc aac gag atc cta ttc ccg ccg aac caa acc ctt      48
82 Met Val Ser Val Phe Asn Glu Ile Leu Phe Pro Pro Asn Gln Thr Leu
83 1 5 10 15
84 ctt cgc ccc tcc ctc cat tcc cca acc tct ttc ttc acc tct ccc act      96
85 Leu Arg Pro Ser Leu His Ser Pro Thr Ser Phe Phe Thr Ser Pro Thr
86 20 25 30
87 cga aaa ttc cct cgc tct cgc cct aac cct att cta cgc tgc tcc att      144
88 Arg Lys Phe Pro Arg Ser Arg Pro Asn Pro Ile Leu Arg Cys Ser Ile
89 35 40 45
90 gcg gag gaa tcc acc gcg tct cgc ccc aaa acc aga gac tcc gcc ccc      192
91 Ala Glu Glu Ser Thr Ala Ser Pro Pro Lys Thr Arg Asp Ser Ala Pro
92 50 55 60
93 gtg gac tgc gtc gtc gtc ggc gga ggc gtc agc ggc ctc tgc atc gcc      240
94 Val Asp Cys Val Val Val Gly Gly Gly Val Ser Gly Leu Cys Ile Ala
95 65 70 75 80
96 cag gcc ctc gcc acc aaa cac gcc aat gcc aac gtc gtc gtc acg gag      288
97 Gln Ala Leu Ala Thr Lys His Ala Asn Ala Asn Val Val Val Thr Glu
98 85 90 95
99 gcc cga gac cgc gtc ggc ggc aac atc acc acg atg gag agg gac gga      336
100 Ala Arg Asp Arg Val Gly Gly Asn Ile Thr Thr Met Glu Arg Asp Gly
101 100 105 110
102 tac ctc tgg gaa gaa ggc ccc aac agc ttc cag cct tct gat cca atg      384
103 Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met
104 115 120 125
105 ctc acc atg gtg gtg gac agt ggt tta aag gat gag ctt gtt ttg ggg      432
106 Leu Thr Met Val Val Asp Ser Gly Leu Lys Asp Glu Leu Val Leu Gly
107 130 135 140
108 gat cct gat gca cct cgg ttt gtg ttg tgg aac agg aag ttg agg ccg      480
109 Asp Pro Asp Ala Pro Arg Phe Val Leu Trp Asn Arg Lys Leu Arg Pro
110 145 150 155 160
111 gtg ccc ggg aag ctg act gat ttg cct ttc ttt gac ttg atg agc att      528
112 Val Pro Gly Lys Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile
113 165 170 175
114 ggt ggc aaa atc agg gct ggc ttt ggt gcg ctt gga att cgg cct cct      576
115 Gly Gly Lys Ile Arg Ala Gly Phe Gly Ala Leu Gly Ile Arg Pro Pro
116 180 185 190
117 cct cca ggt cat gag gaa tcg gtt gaa gag ttt gtt cgt cgg aac ctt      624

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118	Pro	Pro	Gly	His	Glu	Glu	Ser	Val	Glu	Glu	Phe	Val	Arg	Arg	Asn	Leu	
119			195					200					205				
120	ggt	gat	gag	gtt	ttt	gaa	cgg	ttg	ata	gag	cct	ttt	tgt	tca	ggg	gtc	672
121	Gly	Asp	Glu	Val	Phe	Glu	Arg	Leu	Ile	Glu	Pro	Phe	Cys	Ser	Gly	Val	
122		210					215				220						
123	tat	gca	ggc	gat	cct	tca	aaa	tta	agt	atg	aaa	gca	gca	ttc	ggg	aaa	720
124	Tyr	Ala	Gly	Asp	Pro	Ser	Lys	Leu	Ser	Met	Lys	Ala	Ala	Phe	Gly	Lys	
125	225					230					235					240	
126	gtt	tgg	aag	ctg	gaa	aaa	aat	ggt	ggt	agc	att	att	ggt	gga	act	ttc	768
127	Val	Trp	Lys	Leu	Glu	Lys	Asn	Gly	Gly	Ser	Ile	Ile	Gly	Gly	Thr	Phe	
128					245					250					255		
129	aaa	gca	ata	caa	gag	aga	aat	gga	gct	tca	aaa	cca	cct	cga	gat	ccg	816
130	Lys	Ala	Ile	Gln	Glu	Arg	Asn	Gly	Ala	Ser	Lys	Pro	Pro	Arg	Asp	Pro	
131			260					265						270			
132	cgt	ctg	cca	aaa	cca	aaa	ggt	cag	act	ggt	gga	tct	ttc	cgg	aag	gga	864
133	Arg	Leu	Pro	Lys	Pro	Lys	Gly	Gln	Thr	Val	Gly	Ser	Phe	Arg	Lys	Gly	
134			275					280					285				
135	ctt	acc	atg	ttg	cct	gat	gca	att	tct	gcc	aga	cta	ggc	aac	aaa	gta	912
136	Leu	Thr	Met	Leu	Pro	Asp	Ala	Ile	Ser	Ala	Arg	Leu	Gly	Asn	Lys	Val	
137		290					295					300					
138	aag	tta	tct	tgg	aag	ctt	tca	agt	att	agt	aaa	ctg	gat	agt	gga	gag	960
139	Lys	Leu	Ser	Trp	Lys	Leu	Ser	Ser	Ile	Ser	Lys	Leu	Asp	Ser	Gly	Glu	
140	305					310					315				320		
141	tac	agt	ttg	aca	tat	gaa	aca	cca	gaa	gga	gtg	gtt	tct	ttg	cag	tgc	1008
142	Tyr	Ser	Leu	Thr	Tyr	Glu	Thr	Pro	Glu	Gly	Val	Val	Ser	Leu	Gln	Cys	
143					325					330					335		
144	aaa	act	gtt	gtc	ctg	acc	att	cct	tcc	tat	gtt	gct	agt	aca	ttg	ctg	1056
145	Lys	Thr	Val	Val	Leu	Thr	Ile	Pro	Ser	Tyr	Val	Ala	Ser	Thr	Leu	Leu	
146			340					345					350				
147	cgt	cct	ctg	tct	gct	gct	gct	gca	gat	gca	ctt	tca	aag	ttt	tat	tac	1104
148	Arg	Pro	Leu	Ser	Ala	Ala	Ala	Ala	Asp	Ala	Leu	Ser	Lys	Phe	Tyr	Tyr	
149		355					360					365					
150	cct	cca	gtt	gct	gca	gtt	tcc	ata	tcc	tat	cca	aaa	gaa	gct	att	aga	1152
151	Pro	Pro	Val	Ala	Ala	Val	Ser	Ile	Ser	Tyr	Pro	Lys	Glu	Ala	Ile	Arg	
152		370					375					380					
153	tca	gaa	tgc	ttg	ata	gat	ggt	gag	ttg	aag	ggg	ttt	ggt	caa	ttg	cat	1200
154	Ser	Glu	Cys	Leu	Ile	Asp	Gly	Glu	Leu	Lys	Gly	Phe	Gly	Gln	Leu	His	
155	385					390					395				400		
156	cca	cgt	agc	caa	gga	gtg	gaa	aca	tta	gga	act	ata	tac	agc	tca	tca	1248
157	Pro	Arg	Ser	Gln	Gly	Val	Glu	Thr	Leu	Gly	Thr	Ile	Tyr	Ser	Ser	Ser	
158				405						410				415			
159	cta	ttc	ccc	aac	cga	gca	cca	cct	gga	agg	gtt	cta	ctc	ttg	aat	tac	1296
160	Leu	Phe	Pro	Asn	Arg	Ala	Pro	Pro	Gly	Arg	Val	Leu	Leu	Leu	Asn	Tyr	
161			420					425					430				
162	att	gga	gga	gca	act	aat	act	gga	att	tta	tcg	aag	acg	gac	agt	gaa	1344
163	Ile	Gly	Gly	Ala	Thr	Asn	Thr	Gly	Ile	Leu	Ser	Lys	Thr	Asp	Ser	Glu	
164			435					440					445				
165	ctt	gtg	gaa	aca	gtt	gat	cga	gat	ttg	agg	aaa	atc	ctt	ata	aac	cca	1392
166	Leu	Val	Glu	Thr	Val	Asp	Arg	Asp	Leu	Arg	Lys	Ile	Leu	Ile	Asn	Pro	

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167      450      455      460
168 aat gcc cag gat cca ttt gta gtg ggg gtg aga ctg tgg cct caa gct 1440
169 Asn Ala Gln Asp Pro Phe Val Val Gly Val Arg Leu Trp Pro Gln Ala
170 465      470      475      480
171 att cca cag ttc tta gtt ggc cat ctt gat ctt cta gat gtt gct aaa 1488
172 Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu Asp Val Ala Lys
173      485      490      495
174 gct tct atc aga aat act ggg ttt gaa ggg ctc ttc ctt ggg ggt aat 1536
175 Ala Ser Ile Arg Asn Thr Gly Phe Glu Gly Leu Phe Leu Gly Gly Asn
176      500      505      510
177 tat gtg tct ggt gtt gcc ttg gga cga tgc gtt gag gga gcc tat gag 1584
178 Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu
179      515      520      525
180 gta gca gct gaa gta aac gat ttt ctc aca aat aga gtg tac aaa tag 1632
181 Val Ala Ala Glu Val Asn Asp Phe Leu Thr Asn Arg Val Tyr Lys
182      530      535      540      543
184 <210> SEQ ID NO: 6
185 <211> LENGTH: 543
186 <212> TYPE: PRT
187 <213> ORGANISM: Glycine max var. Williams82
189 <400> SEQUENCE: 6
190 Met Val Ser Val Phe Asn Glu Ile Leu Phe Pro Pro Asn Gln Thr Leu
191 1      5      10      15
192 Leu Arg Pro Ser Leu His Ser Pro Thr Ser Phe Phe Thr Ser Pro Thr
193      20      25      30
194 Arg Lys Phe Pro Arg Ser Arg Pro Asn Pro Ile Leu Arg Cys Ser Ile
195      35      40      45
196 Ala Glu Glu Ser Thr Ala Ser Pro Pro Lys Thr Arg Asp Ser Ala Pro
197      50      55      60
198 Val Asp Cys Val Val Val Gly Gly Gly Val Ser Gly Leu Cys Ile Ala
199 65      70      75      80
200 Gln Ala Leu Ala Thr Lys His Ala Asn Ala Asn Val Val Val Thr Glu
201      85      90      95
202 Ala Arg Asp Arg Val Gly Gly Asn Ile Thr Thr Met Glu Arg Asp Gly
203      100      105      110
204 Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met
205      115      120      125
206 Leu Thr Met Val Val Asp Ser Gly Leu Lys Asp Glu Leu Val Leu Gly
207      130      135      140
208 Asp Pro Asp Ala Pro Arg Phe Val Leu Trp Asn Arg Lys Leu Arg Pro
209 145      150      155      160
210 Val Pro Gly Lys Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile
211      165      170      175
212 Gly Gly Lys Ile Arg Ala Gly Phe Gly Ala Leu Gly Ile Arg Pro Pro
213      180      185      190
214 Pro Pro Gly His Glu Glu Ser Val Glu Glu Phe Val Arg Arg Asn Leu
215      195      200      205
216 Gly Asp Glu Val Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val
217      210      215      220

```

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218 Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys
219 225 230 235 240
220 Val Trp Lys Leu Glu Lys Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe
221 245 250 255
222 Lys Ala Ile Gln Glu Arg Asn Gly Ala Ser Lys Pro Pro Arg Asp Pro
223 260 265 270
224 Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly
225 275 280 285
226 Leu Thr Met Leu Pro Asp Ala Ile Ser Ala Arg Leu Gly Asn Lys Val
227 290 295 300
228 Lys Leu Ser Trp Lys Leu Ser Ser Ile Ser Lys Leu Asp Ser Gly Glu
229 305 310 315 320
230 Tyr Ser Leu Thr Tyr Glu Thr Pro Glu Gly Val Val Ser Leu Gln Cys
231 325 330 335
232 Lys Thr Val Val Leu Thr Ile Pro Ser Tyr Val Ala Ser Thr Leu Leu
233 340 345 350
234 Arg Pro Leu Ser Ala Ala Ala Ala Asp Ala Leu Ser Lys Phe Tyr Tyr
235 355 360 365
236 Pro Pro Val Ala Ala Val Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg
237 370 375 380
238 Ser Glu Cys Leu Ile Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His
239 385 390 395 400
240 Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser
241 405 410 415
242 Leu Phe Pro Asn Arg Ala Pro Pro Gly Arg Val Leu Leu Leu Asn Tyr
243 420 425 430
244 Ile Gly Gly Ala Thr Asn Thr Gly Ile Leu Ser Lys Thr Asp Ser Glu
245 435 440 445
246 Leu Val Glu Thr Val Asp Arg Asp Leu Arg Lys Ile Leu Ile Asn Pro
247 450 455 460
248 Asn Ala Gln Asp Pro Phe Val Val Gly Val Arg Leu Trp Pro Gln Ala
249 465 470 475 480
250 Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu Asp Val Ala Lys
251 485 490 495
252 Ala Ser Ile Arg Asn Thr Gly Phe Glu Gly Leu Phe Leu Gly Gly Asn
253 500 505 510
254 Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu
255 515 520 525
256 Val Ala Ala Glu Val Asn Asp Phe Leu Thr Asn Arg Val Tyr Lys
257 530 535 540 543
259 <210> SEQ ID NO: 7
260 <211> LENGTH: 39
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify bchH gene
267 <400> SEQUENCE: 7
268 gacatctagt ctagacgacc atatgcacgg tgaagtctc 39
270 <210> SEQ ID NO: 8

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/697,719

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Input Set : A:\0020-4764P.st25A.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:27; N Pos. 6,7,9,10,12,13,15,16,18,19
Seq#:28; N Pos. 8,9,11,12,14,15,17,18,20,21
Seq#:77; Xaa Pos. 2,4,5

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:9; Line(s) 287
Seq#:10; Line(s) 298
Seq#:11; Line(s) 309
Seq#:12; Line(s) 320
Seq#:13; Line(s) 331
Seq#:14; Line(s) 342
Seq#:19; Line(s) 576
Seq#:20; Line(s) 587
Seq#:21; Line(s) 598
Seq#:22; Line(s) 609
Seq#:27; Line(s) 664
Seq#:28; Line(s) 680
Seq#:29; Line(s) 696
Seq#:30; Line(s) 707
Seq#:31; Line(s) 718
Seq#:32; Line(s) 729
Seq#:33; Line(s) 740
Seq#:34; Line(s) 751
Seq#:35; Line(s) 762
Seq#:36; Line(s) 773
Seq#:37; Line(s) 784
Seq#:38; Line(s) 795
Seq#:39; Line(s) 806
Seq#:40; Line(s) 817
Seq#:41; Line(s) 828
Seq#:42; Line(s) 839
Seq#:43; Line(s) 850
Seq#:44; Line(s) 861
Seq#:45; Line(s) 872
Seq#:46; Line(s) 883
Seq#:47; Line(s) 894
Seq#:48; Line(s) 905
Seq#:49; Line(s) 916
Seq#:50; Line(s) 927
Seq#:51; Line(s) 938
Seq#:52; Line(s) 949